

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 23:21:32 ; Search time 5 Seconds
(without alignments)

261.443 Million cell updates/sec

Perfect score: 1505

Sequence: 1 MRGSEQVLLMWLEVLAVGGT.....SEQIFLEQLGSCCKKDS 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA New:

1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	231.5	15.4	123	6	US-10-821-234-1241
3	176.5	11.7	3002	6	US-10-821-234-916
4	175	11.6	652	6	US-10-821-234-1016
5	165	11.0	1238	7	US-11-078-735-21
6	160.5	10.7	618	7	US-11-078-735-18
7	158.5	10.5	387	7	US-11-137-465-57
8	158	10.5	997	7	US-11-113-424-37
9	156	10.4	999	7	US-11-113-424-36
10	155.5	10.3	961	7	US-11-113-424-35
11	154	10.2	497	6	US-10-821-234-1119
13	153	10.2	1218	7	US-11-078-735-20
14	152.5	10.1	964	7	US-11-137-465-58
15	152.5	10.1	965	7	US-11-113-424-2
16	152.5	10.1	965	7	US-11-147-047-51
17	150	10.0	671	7	US-11-029-003-6
18	150	10.0	671	7	US-11-029-003-6
20	148	9.8	484	7	US-11-078-735-43
22	148	9.8	723	7	US-11-078-735-17
23	146.5	9.7	545	7	US-11-102-240-110
24	145.5	9.7	332	7	US-11-078-735-33
25	145.5	9.7	332	7	US-11-078-735-51
26	145.5	9.7	369	7	US-11-078-735-38
27	145	9.6	1400	6	US-10-821-234-1045
28	144.5	9.6	696	7	US-11-029-003-8
30	141.5	9.4	685	7	US-11-078-735-19
31	141.5	9.4	897	7	US-11-137-465-35

Sequence 36, Appl	7	US-11-137-465-36	993	9.4	141.5	32
Sequence 1076, Ap	6	US-10-821-234-1076	3717	9.3	140	33
Sequence 38, Appl	3	US-11-147-047-38	383	9.3	139.5	35
Sequence 1310, Ap	6	US-10-821-234-1310	986	9.3	139.5	36
Sequence 30, Appl	7	US-11-078-735-30	291	9.2	138.5	37
Sequence 6, Appl	7	US-11-096-051-6	821	9.2	138	38
Sequence 20, Appl	7	US-11-096-051-20	862	9.2	138	39
Sequence 4, Appl	7	US-11-096-051-4	2376	9.2	138	40
Sequence 2, Appl	7	US-11-096-051-2	2715	9.2	138	41
Sequence 10, Appl	7	US-11-096-051-10	2721	9.2	138	42
Sequence 8, Appl	7	US-11-096-051-8	2725	9.2	138	43
Sequence 1412, Ap	6	US-10-821-234-1412	703	9.1	137	44
Sequence 51, Appl	7	US-11-113-424-51	2715	9.1	137	45
Sequence 18, Appl	7	US-11-096-051-18	296	8.9	134.5	47
Sequence 39, Appl	7	US-11-113-424-39	956	8.7	130.5	48
Sequence 52, Appl	7	US-11-113-424-52	2725	8.5	127.5	49
Sequence 12, Appl	7	US-11-096-051-12	257	8.4	126	50
Sequence 1216, Ap	6	US-10-821-234-1216	143	8.3	125	51
Sequence 16, Appl	7	US-11-067-121-16	757	8.3	124	52
Sequence 14, Appl	7	US-11-113-424-14	2769	8.2	124	53
Sequence 53, Appl	7	US-11-113-424-53	2515	8.1	122	54
Sequence 1236, Ap	6	US-10-821-234-1236	112	8.0	121	55
Sequence 28, Appl	7	US-11-113-424-28	720	7.7	116.5	56
Sequence 26, Appl	7	US-11-113-424-26	747	7.7	116.5	57
Sequence 1164, Ap	6	US-10-821-234-1164	765	7.6	115	58
Sequence 6, Appl	7	US-11-067-121-6	755	7.4	112	60
Sequence 2, Appl	6	US-10-945-853-2	188	7.3	109.5	61
Sequence 1155, Ap	6	US-10-821-234-1155	4419	7.3	109.5	62
Sequence 1, Appl	6	US-10-831-997-4	961	7.2	108.5	64
Sequence 2, Appl	6	US-10-945-853-1	188	7.1	107.5	65
Sequence 1116, Ap	7	US-11-108-775-2	3500	7.0	106	67
Sequence 8, Appl	6	US-10-478-345-8	321	6.3	96	68
Sequence 86, Appl	6	US-11-108-528-86	1613	6.2	93.5	69
Sequence 4, Appl	6	US-10-478-345-4	336	6.2	93	70
Sequence 2, Appl	6	US-10-478-345-2	354	6.1	92.5	72
Sequence 17, Appl	6	US-11-067-121-17	1018	6.1	92.5	73
Sequence 110, App	6	US-10-986-501-110	457	6.0	91	74
Sequence 84, Appl	7	US-11-108-528-84	1613	6.0	91	75
Sequence 184, App	6	US-11-113-424-184	126	5.8	88	76
Sequence 2, Appl	6	US-10-831-997-2	1170	5.8	88	77
Sequence 28, Appl	7	US-11-046-456-28	1170	5.8	88	78
Sequence 28, Appl	7	US-11-046-644-28	1170	5.8	88	79
Sequence 38, Appl	7	US-11-076-187-2	468	5.8	87.5	80
Sequence 1068, Ap	6	US-11-102-240-38	720	5.8	87.5	81
Sequence 1, Appl	6	US-11-108-172-1068	5179	5.8	87	82
Sequence 46, Appl	6	US-10-844-035-1	372	5.7	86	84
Sequence 1063, Ap	6	US-10-980-388-46	575	5.7	86	85
Sequence 114, App	6	US-10-821-234-1063	486	5.7	85.5	87
Sequence 110, App	7	US-11-092-140-114	411	5.6	85	88
Sequence 6, Appl	7	US-11-092-140-110	488	5.6	85	89
Sequence 7, Appl	6	US-10-478-345-6	357	5.6	84.5	90
Sequence 1300, Ap	6	US-10-821-234-1300	1028	5.6	84	91
Sequence 40, Appl	6	US-10-980-388-40	280	5.5	83.5	92
Sequence 5, Appl	6	US-11-076-187-5	544	5.5	83	93
Sequence 30, Appl	6	US-10-967-527A-30	308	5.5	82.5	94
Sequence 70, Appl	7	US-11-113-424-70	620	5.5	82.5	95
Sequence 2, Appl	6	US-11-139-499-2	234	5.4	82	97
Sequence 1532, Ap	6	US-10-821-234-1532	705	5.4	82	98
Sequence 82, Appl	7	US-11-108-528-82	1615	5.4	81.5	99
Sequence 7, Appl	7	US-11-021-441-7	502	5.4	81	100
Sequence 9, Appl	7	US-11-021-441-9	563	5.4	81	101
Sequence 15, Appl	7	US-11-021-441-15	574	5.4	81	102
Sequence 11, Appl	7	US-11-021-441-11	581	5.4	81	103
Sequence 13, Appl	7	US-11-021-441-13	581	5.4	81	104
Sequence 4, Appl	6	US-10-821-234-1539	165	5.3	80.5	106
Sequence 1539, Ap	6	US-10-821-234-1539	350	5.3	80.5	107
Sequence 4, Appl	7	US-11-153-880-4	419	5.3	80.5	108
Sequence 2, Appl	7	US-11-064-769-2	419	5.3	80.5	109
Sequence 1357, Ap	6	US-10-821-234-1357	405	5.3	80	111

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OM protein - protein search, using sw model

Run on: December 3, 2005, 23:21:27 ; Search time 66 Seconds
(without alignments)

1728.294 Million cell updates/sec

Perfect score: 1505

Sequence: 1 MRGSQEVLLMWLLVLA VGT.....SEQISFLEEQLGSCSCKKDS 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326

Total number of hits satisfied

Enfance et jeunesse

Maximum DB seq length: 2000000000

1. *Chlorophyll a* (Chl *a*)

Post-processing: Minimum Match 0%

Listing first 1500 summaries

Database : Published Announcements in Manuscript

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Database : PUBLISHED_APPLICATIONS_AA_MAIN:
1: /cgn2_6/ptodata/1/pubnbaa/u1s07 PUBCOMB pen:*
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2: /cgndata/1/pubaa/US08_PUBCOMB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.per:

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5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.per:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1505	100.0	273	3	US-09-790-264-10	Sequence 10, Appl
75	1505	100.0	273	4	US-10-167-749-506	Sequence 506, App
76	1505	100.0	273	4	US-10-167-749-508	Sequence 508, App
125	1505	100.0	273	4	US-10-219-085-178	Sequence 178, App
151	1505	100.0	273	4	US-10-269-353-10	Sequence 10, Appl
241	1505	100.0	273	4	US-10-170-481A-506	Sequence 506, App
242	1505	100.0	273	4	US-10-170-481A-508	Sequence 508, App
245	1505	100.0	273	4	US-10-210-028-506	Sequence 506, App
246	1505	100.0	273	4	US-10-210-028-508	Sequence 508, App
255	1505	100.0	273	4	US-10-162-521A-506	Sequence 506, App
256	1505	100.0	273	4	US-10-162-521A-508	Sequence 508, App
281	1505	100.0	273	4	US-10-287-971-102	Sequence 102, App
286	1505	100.0	273	5	US-10-918-851-506	Sequence 506, App
287	1505	100.0	273	5	US-10-918-851-508	Sequence 508, App
288	1505	100.0	273	5	US-10-900-926-10	Sequence 10, Appl
289	1505	100.0	273	5	US-10-805-667-506	Sequence 506, App
290	1505	100.0	273	5	US-10-805-667-508	Sequence 508, App
291	1505	100.0	273	5	US-10-897-359-506	Sequence 506, App
292	1505	100.0	273	5	US-10-897-359-508	Sequence 508, App
293	1505	100.0	273	5	US-10-893-802-506	Sequence 506, App
294	1505	100.0	273	5	US-10-893-802-508	Sequence 508, App
295	1505	100.0	273	5	US-10-897-360-506	Sequence 506, App
296	1505	100.0	273	5	US-10-897-360-508	Sequence 508, App
299	1505	100.0	273	6	US-11-129-762-506	Sequence 506, App
300	1505	100.0	273	6	US-11-129-762-508	Sequence 508, App
325	1504	99.9	273	3	US-09-852-472-2	Sequence 2, Appl
336	1504	99.9	273	4	US-10-167-749-510	Sequence 510, App
372	1504	99.9	273	4	US-10-170-481A-510	Sequence 510, App

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OM protein - protein search, using sw model

Run on: December 3, 2005, 23:18:21 ; Search time 24 Seconds

(without alignments)
940.436 Million cell updates/sec

Perfect score: 1505
Sequence: 1 MRGSQVLLMWLLVAVGGT.....SEQISFLEQLGSCCKKDS 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA:
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3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCRUS COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
9	1180	78.4	278	2	US-09-724-864-52
10	254.5	16.9	553	2	US-09-249-697A-6
11	254.5	16.9	553	2	US-09-363-316B-6
12	254.5	16.9	553	2	US-10-136-227A-6
13	254.5	16.9	553	2	US-09-981-649A-6
14	254.5	16.8	284	2	US-09-312-283C-389
17	251.5	16.7	553	2	US-09-249-697A-19
18	251.5	16.7	553	2	US-09-363-316B-24
19	251.5	16.7	553	2	US-10-136-227A-24
20	251.5	16.7	553	2	US-09-981-649A-24
21	251.5	16.7	554	2	US-10-136-227A-32
22	251.5	16.7	554	2	US-09-981-649A-32
23	251.5	16.7	594	2	US-09-949-016-8175
24	249.5	16.6	554	2	US-10-136-227A-30
25	249.5	16.6	554	2	US-09-981-649A-30
26	249.5	16.6	559	2	US-10-136-227A-28
27	249.5	16.6	559	2	US-09-981-649A-28
41	216.5	14.4	502	2	US-09-363-316B-18
42	216.5	14.4	502	2	US-10-136-227A-18
43	216.5	14.4	502	2	US-09-981-649A-18
44	216.5	14.4	537	2	US-09-249-697A-4
45	216.5	14.4	537	2	US-09-363-316B-4
46	216.5	14.4	537	2	US-10-136-227A-4
47	216.5	14.4	537	2	US-09-981-649A-4
48	215.5	14.3	100	2	US-09-249-697A-3
49	215.5	14.3	100	2	US-09-363-316B-3
50	215.5	14.3	100	2	US-10-136-227A-3
51	215.5	14.3	100	2	US-09-981-649A-3

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189	12.6	678	1	US-08-435-436-2	Sequence 2, Appli
189	12.6	678	1	US-08-438-863-2	Sequence 2, Appli
189	12.6	678	1	US-08-438-864-2	Sequence 2, Appli
189	12.6	678	2	US-08-438-862-2	Sequence 2, Appli
189	12.6	678	2	US-08-628-747-2	Sequence 2, Appli
189	12.6	678	2	US-08-402-253-2	Sequence 2, Appli
189	12.6	678	2	US-08-443-866B-2	Sequence 2, Appli
184	12.2	673	1	US-08-282-141-3	Sequence 3, Appli
184	12.2	673	1	US-08-435-434-1	Sequence 1, Appli
184	12.2	673	1	US-08-435-436-1	Sequence 1, Appli
184	12.2	673	1	US-08-438-863-1	Sequence 1, Appli
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184	12.2	673	2	US-08-438-862-1	Sequence 1, Appli
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184	12.2	673	2	US-08-402-253-1	Sequence 1, Appli
184	12.2	673	2	US-08-443-866B-1	Sequence 1, Appli
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182.5	12.1	816	2	US-09-661-468-37	Sequence 37, Appli
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182	12.1	810	2	US-09-055-699-34	Sequence 34, Appli
182	12.1	810	2	US-09-273-565-34	Sequence 34, Appli
182	12.1	810	2	US-09-565-538-34	Sequence 34, Appli
182	12.1	810	2	US-09-661-468-34	Sequence 34, Appli
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176.5	11.7	1935	2	US-09-949-016-10403	Sequence 10403, A
176.5	11.7	281	2	US-09-538-092-1076	Sequence 1076, Ap
176	11.7	1581	2	US-09-949-002-414	Sequence 414, App
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175	11.6	652	1	US-08-751-305-2	Sequence 2, Appli
175	11.6	1587	2	US-09-949-002-354	Sequence 354, App
175	11.6	2703	1	US-08-185-432-19	Sequence 19, Appl
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175	11.6	2703	2	US-09-121-457-4	Sequence 4, Appli
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173.5	11.5	1247	2	US-09-961-403-14	Sequence 14, Appli
173	11.5	4588	2	US-10-025-225-8	Sequence 8, Appli
172.5	11.5	1833	2	US-08-479-722B-2	Sequence 2, Appli
172.5	11.5	1833	2	US-09-592-685-2	Sequence 2, Appli
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168	11.2	1193	2	US-09-195-524-10	Sequence 10, Appli
168	11.2	1193	2	US-09-310-685-8	Sequence 8, Appli
166	11.0	832	2	US-08-981-392-6	Sequence 6, Appli
166	11.0	832	2	US-09-908-322-6	Sequence 8, Appli
165	11.0	1065	1	US-08-400-159-8	Sequence 8, Appli
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165	11.0	1238	2	US-09-214-278-5	Sequence 5, Appli
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U'Hare, L.
09/19/78/191
Seq ID 506
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